

CLAIMS

1. An isolated polynucleotide which encodes a protein comprising the amino acid sequence of SEQ ID NO:2.
2. The isolated polynucleotide of Claim 1, wherein said
5 protein has LysR3 transcriptional regulatory activity.
3. An isolated polynucleotide, which comprises SEQ ID NO:1.
4. An isolated polynucleotide which is complimentary to the polynucleotide of Claim 3.
5. An isolated polynucleotide which is at least 70%
10 identical to the polynucleotide of Claim 3.
6. An isolated polynucleotide which is at least 80% identical to the polynucleotide of Claim 3.
7. An isolated polynucleotide which is at least 90% identical to the polynucleotide of Claim 3.
8. An isolated polynucleotide which hybridizes under
15 stringent conditions to the polynucleotide of Claim 3; wherein said stringent conditions comprise washing in 5X SSC at a temperature from 50 to 68°C.
9. The isolated polynucleotide of Claim 3, which encodes a
20 protein having LysR3 transcriptional regulatory activity.
10. An isolated polynucleotide which comprises at least 15 consecutive nucleotides of the polynucleotide of Claim 3.
11. The isolated polynucleotide of Claim 10 which
25 comprises SEQ ID NO:3.
12. A vector comprising the isolated polynucleotide of Claim 1.

13. A vector comprising the isolated polynucleotide of Claim 3.
14. A host cell comprising the isolated polynucleotide of Claim 1.
- 5 15. A host cell comprising the isolated polynucleotide of Claim 3.
16. The host cell of Claim 14, which is a *Coryneform* bacterium.
17. The host cell of Claim 15, which is a *Coryneform* bacterium.
- 10 18. The host cell of Claim 14, wherein said host cell is selected from the group consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, *Brevibacterium divaricatum*.
- 15 19. The host cell of Claim 14, wherein said host cell is selected from the group consisting of *Coryneform glutamicum* ATCC13032, *Corynebacterium acetoglutamicum* ATCC15806, *Corynebacterium acetoacidophilum* ATCC13870, *Corynebacterium melassecola* ATCC17965, *Corynebacterium thermoaminogenes* FERM BP-1539, *Brevibacterium flavum* ATCC14067, *Brevibacterium lactofermentum* ATCC13869, *Brevibacterium divaricatum* ATCC14020.
- 20 25 20. The host cell of Claim 15, wherein said host cell is selected from the group consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, *Brevibacterium divaricatum*.
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21. The host cell of Claim 15, wherein said host cell is selected from the group consisting of *Coryneform glutamicum* ATCC13032, *Corynebacterium acetoglutamicum* ATCC15806, *Corynebacterium acetoacidophilum* ATCC13870, 5 *Corynebacterium melassecola* ATCC17965, *Corynebacterium thermoaminogenes* FERM BP-1539, *Brevibacterium flavum* ATCC14067, *Brevibacterium lactofermentum* ATCC13869, *Brevibacterium divaricatum* ATCC14020.
22. A *Coryneform* bacterium which comprises an attenuated 10 *lysR3* gene.
23. The *Coryneform* bacterium of Claim 22, wherein said *lysR3* gene comprises the polynucleotide sequence of SEQ ID NO:1.
24. The *Coryneform* bacterium of Claim 27, wherein said 15 *lysR3* gene comprises the polynucleotide sequence of SEQ ID NO:3.
25. *Coryneform glutamicum* DSM 13618.
26. A process for producing L-amino acids comprising 20 culturing a bacterial cell in a medium suitable for producing L-amino acids, wherein said bacterial cell comprises an attenuated *lysR3* gene.
27. The process of Claim 26, wherein said bacterial cell is a *Coryneform* bacterium or *Brevibacterim*.
28. The process of Claim 26, wherein said bacterial cell 25 is selected from the group consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, 30 *Brevibacterium divaricatum*.
29. The process of Claim 26, wherein said bacterial cell is selected from the group consisting of *Coryneform*

glutamicum ATCC13032, *Corynebacterium acetoglutamicum*
ATCC15806, *Corynebacterium acetoacidophilum* ATCC13870,
Corynebacterium melassecola ATCC17965, *Corynebacterium*
thermoaminogenes FERM BP-1539, *Brevibacterium flavum*
5 ATCC14067, *Brevibacterium lactofermentum* ATCC13869,
Brevibacterium divaricatum ATCC14020.

30. The process of Claim 26, wherein said lysR3 gene
comprises the polynucleotide sequence of SEQ ID NO:1.
31. The process of Claim 26, wherein said lysR3 gene
10 comprises the polynucleotide sequence of SEQ ID NO:3.
32. The process of Claim 26, wherein said L-amino acid is
L-lysine.
33. The process of Claim 32, wherein said bacterial cell
is selected from the group consisting of *Corynebacterium*
15 *glutamicum* FERM-P1709, *Brevibacterium flavum* FERM-
P1708, *Brevibacterium lactofermentum* FERM-
P1712, *Corynebacterium glutamicum* FERM-P6463,
Corynebacterium glutamicum FERM-P6464, *Corynebacterium*
glutamicum DM58-1, *Corynebacterium glutamicum* DG52-5,
20 *Corynebacterium glutamicum* DSM 5714, and *Corynebacterium*
glutamicum DSM 12866.
34. The process of Claim 26, wherein said L-amino acid is
L-valine.
35. The process of Claim 33, wherein said bacterial cell
25 is selected from the group consisting of *Corynebacterium*
glutamicum DSM-12455, *Corynebacterium glutamicum* FERM-P
9324, *Brevibacterium lactofermentum* FERM-P9324, and
Brevibacterium lactofermentum FERM-BP 1763.
36. The process of Claim 32, wherein said bacteria further
30 comprises at least one gene whose expression is
enhanced, wherein said gene is selected from the group
consisting of *dapA*, *eno*, *zwf*, *pyc*, and *lysE*.

37. The process of Claim 32, wherein said bacteria further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of pck, pgi, and poxB.
- 5 38. The process of Claim 26, wherein said bacteria further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of ilvBN, ilvD and mgo.
- 10 39. A process for screening for polynucleotides which encode a protein having LysR3 transcriptional regulatory activity comprising hybridizing the isolated polynucleotide of Claim 1 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of LysR3
15 transcriptional regulatory activity in said protein.
- 20 40. A process for screening for polynucleotides which encode a protein having LysR3 transcriptional regulatory activity comprising hybridizing the isolated polynucleotide of Claim 3 to the polynucleotide to be screened; expressing the polynucleotide to produce a protein; and detecting the presence or absence of LysR3 transcriptional regulatory activity in said protein.
- 25 41. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.
- 30 42. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 1, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive nucleotides of the complement thereof.

43. A method for detecting a nucleic acid with at least
70% homology to nucleotide of Claim 3, comprising
contacting a nucleic acid sample with a probe or primer
comprising at least 15 consecutive nucleotides of the
5 nucleotide sequence of Claim 3, or at least 15
consecutive nucleotides of the complement thereof.
44. A method for producing a nucleic acid with at least
70% homology to nucleotide of Claim 3, comprising
contacting a nucleic acid sample with a primer
10 comprising at least 15 consecutive nucleotides of the
nucleotide sequence of Claim 3, or at least 15
consecutive nucleotides of the complement thereof.
45. A method for making LysR3 protein, comprising:
culturing the host cell of Claim 14 for a time and under
15 conditions suitable for expression of LysR3 protein, and
collecting the LysR3 protein.
46. A method for making LysR3 protein, comprising:
culturing the host cell of Claim 15 for a time and under
conditions suitable for expression of LysR3 protein, and
20 collecting the LysR3 protein.